

SEQUENCE LISTING

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<120> COMPOUNDS HAVING LECTINIC PROPERTIES AND THEIR
 BIOLOGICAL APPLICATIONS

<130> 040388/0113

<140> US 09/077,606

<141> 1998-07-30

<150> WO PCT/FR96/01937

<151> 1996-12-04

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<170> PatentIn Ver. 2.0

<210> 1

<211> 1831

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (62)..(1468)

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Met Ser Ile His Phe Ser Ser Pro Val Phe Thr Ser Arg Ser Ala Ala

1

5

10

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ttc tcg ggc cgc gcc ggc cag gtg cgc ctg agc tcc gct cgc ccc gcc 157

Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro Gly

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ggc ctt ggc agc agc agc ctc tac ggc ctc ggc gcc tcg cgg ccg cgc 205

Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg

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gtg gcc gtg cgc tct gcc tat ggg ggc ccg gtg ggc gcc ggc atc cgc 253

Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg

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gag gtc acc att aac cag agc ctg ctg gcc ccg ctg cgg ctg ggc gcc 301

Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Gly Ala

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gac ccc ttc tcc cag cgg gtg cgc cag gag gag agc gag cag atc aag 349

Asp Pro Phe Ser Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile Lys

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acc ctc aac aac aag ttt gcc tcc ttc atc gac aag gtg cgg ttt ctg 397

Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu

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115 120 125	
cag aag tcg gcc aag agc agc cgc ctc cca gac atc ttt gag gcc cag	493
Gln Lys Ser Ala Lys Ser Ser Arg Leu Pro Asp Ile Phe Glu Ala Gln	
130 135 140	
att gct ggc ctt cgg ggt cag ctt gag gca atg cag gtg gat ggg ggc	541
Ile Ala Gly Leu Arg Gly Gln Leu Glu Ala Met Gln Val Asp Gly Gly	
145 150 155 160	
cgc ctg gag cag ggg ctg cgg acg atg cag gat gtg gtg gag gac ttc	589
Arg Leu Glu Gln Gly Leu Arg Thr Met Gln Asp Val Val Glu Asp Phe	
165 170 175	
aag aat aag tac gaa gat gaa att aac cgc cgc aca gct gct gag aat	637
Lys Asn Lys Tyr Glu Asp Glu Ile Asn Arg Arg Thr Ala Ala Glu Asn	
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gag ttt gtg gtc ctg aag aag gat gtg gat gct gcc tac atg agc aag	685
Glu Phe Val Val Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Ser Lys	
195 200 205	
gtg gag ctg gag gcc aag gtg gat gcc ctg aat gat gag atc aac ttc	733
Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asn Asp Glu Ile Asn Phe	
210 215 220	
ctc agg acc ctc aat gag acg gag ttg aca gag ctt cag tcc cag atc	781
Leu Arg Thr Leu Asn Glu Thr Glu Leu Thr Glu Leu Gln Ser Gln Ile	
225 230 235 240	
tcc gac aca tct gtg gtg ctg tcc atg gac aac agt cgc tcc ctg gac	829
Ser Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp	
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ctg gac ggc atc atc gct gag gtc aag gcg cag tat gag gag atg gcc	877
Leu Asp Gly Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Glu Met Ala	
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aaa tgc agc cgg gct gag gct gaa gcc tgg tac cag acc aag ttt gag	925
Lys Cys Ser Arg Ala Glu Ala Glu Ala Trp Tyr Gln Thr Lys Phe Glu	
275 280 285	
acc ctc cag gcc cag gct ggg aag cat ggg gac gac ctc cgg aat acc	973
Thr Leu Gln Ala Gln Ala Gly Lys His Gly Asp Asp Leu Arg Asn Thr	
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Arg Asn Glu Ile Ser Glu Met Asn Arg Ala Ile Gln Arg Leu Gln Ala	
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Glu Ile Asp Asn Ile Lys Asn Gln Arg Ala Lys Leu Glu Ala Ala Ile	
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Ala Glu Ala Glu Glu Arg Gly Glu Leu Ala Leu Lys Asp Ala Arg Ala	
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Lys Gln Glu Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met	
355 360 365	

gca cgg cag ctg cgt gag tac cag gaa ctc atg agc gtg aag ctg gcc 1213
 Ala Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Ser Val Lys Leu Ala
 370 375 380

ctg gac atc gag atc gcc acc tac cgc aag ctg ctg gag ggc gag gag 1261
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agc cgg ttg gct gga gat gga gtg gga gcc gcc aat atc tct gtg atg 1309
 Ser Arg Leu Ala Gly Asp Gly Val Gly Ala Ala Asn Ile Ser Val Met
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aat tcc act ggt ggc agc agc agt ggc ggt ggc att ggg ctg acc ctc 1357
 Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile Gly Leu Thr Leu
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ggg gga acc atg ggc agc aat gcc ctg agc ttc tcc agc agt gcg ggt 1405
 Gly Gly Thr Met Gly Ser Asn Ala Leu Ser Phe Ser Ser Ser Ala Gly
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cct ggg ctc ctg aag gct tat tcc atc cgg acc gca tcc gcc agt cgc 1453
 Pro Gly Leu Leu Lys Ala Tyr Ser Ile Arg Thr Ala Ser Ala Ser Arg
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agg agt acc cgc gac tgagtgcct cccaccactc cactcctcca gccaccaccc 1508
 Arg Ser Thr Arg Asp
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acaatcacag ccattgccga ggctgaggag tgtggggagc tggcgctcaa ggatgctcgt 1568

gccaaagcagg aggagctgga agccgccctg cagcggggcca agcaggatat ggcacggcag 1628

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 Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro Gly
 20 25 30

ggc ctt ggc agc agc agc ctc tac ggc ctc ggc gcc tcg cgg ccg cgc 144
 Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg
 35 40 45

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gtg gcc gtg cgc tct gcc tat ggg ggc ccg gtg ggc gcc ggc atc cgc 192
Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg
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gag gtc acc att aac cag agc ctg ctg gcc ccg ctg cgg ctg ggc gcc 240
Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Gly Ala
    65                70                75                80

gac ccc ttc tcc cag cgg gtg cgc cag gag gag agc gag cag atc aag 288
Asp Pro Phe Ser Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile Lys
                85                90                95

acc ctc aac aac aag ttt gcc tcc ttc atc gac aag gtg cgg ttt ctg 336
Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu
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gag cag cag aac aag ctg ctg gag acc aag tgg acg ctg ctg cag gag 384
Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu
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Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg
    35                40                45

Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg
    50                55                60

Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Gly Ala
    65                70                75                80

Asp Pro Phe Ser Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile Lys
                85                90                95

Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu
    100                105                110

Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu
    115                120                125

Gln Lys Ser Ala Lys Ser Ser Arg Leu Pro Asp Ile Phe Glu Ala Gln
    130                135                140

Ile Ala Gly Leu Arg Gly Gln Leu Glu Ala Met Gln Val Asp Gly Gly
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Arg Leu Glu Gln Gly Leu Arg Thr Met Gln Asp Val Val Glu Asp Phe
    165                170                175

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Lys Asn Lys Tyr Glu Asp Glu Ile Asn Arg Arg Thr Ala Ala Glu Asn
 180 185 190
 Glu Phe Val Val Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Ser Lys
 195 200 205
 Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asn Asp Glu Ile Asn Phe
 210 215 220
 Leu Arg Thr Leu Asn Glu Thr Glu Leu Thr Glu Leu Gln Ser Gln Ile
 225 230 235
 Ser Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp
 245 250 255
 Leu Asp Gly Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Glu Met Ala
 260 265 270
 Lys Cys Ser Arg Ala Glu Ala Glu Ala Trp Tyr Gln Thr Lys Phe Glu
 275 280 285
 Thr Leu Gln Ala Gln Ala Gly Lys His Gly Asp Asp Leu Arg Asn Thr
 290 295 300
 Arg Asn Glu Ile Ser Glu Met Asn Arg Ala Ile Gln Arg Leu Gln Ala
 305 310 315 320
 Glu Ile Asp Asn Ile Lys Asn Gln Arg Ala Lys Leu Glu Ala Ala Ile
 325 330 335
 Ala Glu Ala Glu Glu Arg Gly Glu Leu Ala Leu Lys Asp Ala Arg Ala
 340 345 350
 Lys Gln Glu Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met
 355 360 365
 Ala Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Ser Val Lys Leu Ala
 370 375 380
 Leu Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu
 385 390 395 400
 Ser Arg Leu Ala Gly Asp Gly Val Gly Ala Ala Asn Ile Ser Val Met
 405 410 415
 Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile Gly Leu Thr Leu
 420 425 430
 Gly Gly Thr Met Gly Ser Asn Ala Leu Ser Phe Ser Ser Ser Ala Gly
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 Pro Gly Leu Leu Lys Ala Tyr Ser Ile Arg Thr Ala Ser Ala Ser Arg
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 Arg Ser Thr Arg Asp
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 Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg
 35 40 45
 Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg
 50 55 60
 Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Gly Ala
 65 70 75 80
 Asp Pro Phe Ser Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile Lys
 85 90 95
 Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu
 100 105 110
 Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu
 115 120 125
 Gln Lys Ser Ala Lys Ser Ser
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